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RAW SEQUENCE LISTING

DATE: 09/18/2002

PATENT APPLICATION: US/09/996,611B

TIME: 15:42:41

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\09182002\I996611B.raw

1 <110> APPLICANT: Chou, Min-Yuan
 2 Leu, Charng-Yih
 4 <120> TITLE OF INVENTION: Novel Human alpha 1 Chain Collagen
 6 <130> FILE REFERENCE: 32350-176844
 8 <140> CURRENT APPLICATION NUMBER: US 09/996,611B
 C--> 9 <141> CURRENT FILING DATE: 2002-09-11
 11 <150> PRIOR APPLICATION NUMBER: TAIWAN 89128027
 12 <151> PRIOR FILING DATE: 2000-12-27
 14 <160> NUMBER OF SEQ ID NOS: 5
 16 <170> SOFTWARE: Microsoft Word
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 954
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Homo sapiens
 23 <220> FEATURE:
 24 <223> OTHER INFORMATION: alpha 1 chain collagen
 25 Pro in this sequence stands for hydroxyproline
 27 <400> SEQUENCE: 1
 28 Met Ala His Tyr Ile Thr Phe Leu Cys Met Val Leu Val Leu Leu
 29 1 5 10 15
 31 Leu Gln Asn Ser Val Leu Ala Glu Asp Gly Glu Val Arg Ser Ser
 32 20 25 30
 34 Cys Arg Thr Ala Pro Thr Asp Leu Val Phe Ile Leu Asp Gly Ser
 35 35 40 45
 37 Tyr Ser Val Gly Pro Glu Asn Phe Glu Ile Val Lys Lys Trp Leu
 38 50 55 60
 40 Val Asn Ile Thr Lys Asn Phe Asp Ile Gly Pro Lys Phe Ile Gln
 41 65 70 75
 43 Val Gly Val Val Gln Tyr Ser Asp Tyr Pro Val Leu Glu Ile Pro
 44 80 85 90
 46 Leu Gly Ser Tyr Asp Ser Gly Glu His Leu Thr Ala Ala Val Glu
 47 95 100 105
 49 Ser Ile Leu Tyr Leu Gly Gly Asn Thr Lys Thr Gly Lys Ala Ile
 50 110 115 120
 52 Gln Phe Ala Leu Asp Tyr Leu Phe Ala Lys Ser Ser Arg Phe Leu
 53 125 130 135
 55 Thr Lys Ile Ala Val Val Leu Thr Asp Gly Lys Ser Gln Asp Asp
 56 140 145 150
 58 Val Lys Asp Ala Ala Gln Ala Ala Arg Asp Ser Lys Ile Thr Leu
 59 155 160 165
 61 Phe Ala Ile Gly Val Gly Ser Glu Thr Glu Asp Ala Glu Leu Arg
 62 170 175 180
 64 Ala Ile Ala Asn Lys Pro Ser Ser Thr Tyr Val Phe Tyr Val Glu

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65		185		190		195
67	Asp Tyr Ile Ala	Ile Ser Lys Ile Arg	Glu Val Met Lys Gln	Lys		
68		200		205		210
70	Leu Cys Glu Glu	Ser Val Cys Pro Thr	Arg Ile Pro Val Ala	Ala		
71		215		220		225
73	Arg Asp Glu Arg	Gly Phe Asp Ile Leu	Leu Gly Leu Asp Val	Asn		
74		230		235		240
76	Lys Lys Val Lys	Lys Arg Ile Gln Leu	Ser Pro Lys Lys Ile	Lys		
77		245		250		255
79	Gly Tyr Glu Val	Thr Ser Lys Val Asp	Leu Ser Glu Leu Thr	Ser		
80		260		265		270
82	Asn Val Phe Pro	Glu Gly Leu Pro Pro	Ser Tyr Val Phe Val	Ser		
83		275		280		285
85	Thr Gln Arg Phe	Lys Val Lys Lys Ile	Trp Asp Leu Trp Arg	Ile		
86		290		295		300
88	Leu Thr Ile Asp	Gly Arg Pro Gln Ile	Ala Val Thr Leu Asn	Gly		
89		305		310		315
91	Val Asp Lys Ile	Leu Leu Phe Thr Thr	Thr Ser Val Ile Asn	Gly		
92		320		325		330
94	Ser Gln Val Val	Thr Phe Ala Asn Pro	Gln Val Lys Thr Leu	Phe		
95		335		340		345
97	Asp Glu Gly Trp	His Gln Ile Arg Leu	Leu Val Thr Glu Gln	Asp		
98		350		355		360
100	Val Thr Leu Tyr	Ile Asp Asp Gln Gln	Ile Glu Asn Lys Pro	Leu		
101		365		370		375
103	His Pro Val Leu	Gly Ile Leu Ile Asn	Gly Gln Thr Gln Ile	Gly		
104		380		385		390
106	Lys Tyr Ser Gly	Lys Glu Glu Thr Val	Gln Phe Asp Val Gln	Lys		
107		395		400		405
109	Leu Arg Ile Tyr	Cys Asp Pro Glu Gln	Asn Asn Arg Glu Thr	Ala		
110		410		415		420
112	Cys Glu Ile Pro	Gly Phe Cys Leu Asn	Gly Pro Ser Asp Val	Gly		
113		425		430		435
115	Ser Thr Pro Ala	Pro Cys Ile Cys Pro	Pro Gly Lys Pro Gly	Leu		
116		440		445		450
118	Gln Gly Pro Lys	Gly Asp Pro Gly Leu	Pro Gly Asn Pro Gly	Tyr		
119		455		460		465
121	Pro Gly Gln Pro	Gly Gln Asp Gly Lys	Pro Gly Tyr Gln Gly	Ile		
122		470		475		480
124	Ala Gly Thr Pro	Gly Val Pro Gly Ser	Pro Gly Ile Gln Gly	Ala		
125		485		490		495
127	Arg Gly Leu Pro	Gly Tyr Lys Gly Glu	Pro Gly Arg Asp Gly	Asp		
128		500		505		510
130	Lys Gly Asp Arg	Gly Leu Pro Gly Phe	Pro Gly Leu His Gly	Met		
131		515		520		525
133	Pro Gly Ser Lys	Gly Glu Met Gly Ala	Lys Gly Asp Lys Gly	Ser		
134		530		535		540
136	Pro Gly Phe Tyr	Gly Lys Lys Gly Ala	Lys Gly Glu Lys Gly	Asn		
137		545		550		555

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139	Ala	Gly	Phe	Pro	Gly	Leu	Pro	Gly	Pro	Ala	Gly	Glu	Pro	Gly	Arg
140					560					565					570
142	His	Gly	Lys	Asp	Gly	Leu	Met	Gly	Ser	Pro	Gly	Phe	Lys	Gly	Glu
143					575					580					585
145	Ala	Gly	Ser	Pro	Gly	Ala	Pro	Gly	Gln	Asp	Gly	Thr	Arg	Gly	Glu
146					590					595					600
148	Pro	Gly	Ile	Pro	Gly	Phe	Pro	Gly	Asn	Arg	Gly	Leu	Met	Gly	Gln
149					605					610					615
151	Lys	Gly	Glu	Ile	Gly	Pro	Pro	Gly	Gln	Gln	Gly	Lys	Lys	Gly	Ala
152					620					625					630
154	Pro	Gly	Met	Pro	Gly	Leu	Met	Gly	Ser	Asn	Gly	Ser	Pro	Gly	Gln
155					635					640					645
157	Pro	Gly	Thr	Pro	Gly	Ser	Lys	Gly	Ser	Lys	Gly	Glu	Pro	Gly	Ile
158					650					655					660
160	Gln	Gly	Met	Pro	Gly	Ala	Ser	Gly	Leu	Lys	Gly	Glu	Pro	Gly	Ala
161					665					670					675
163	Thr	Gly	Ser	Pro	Gly	Glu	Pro	Gly	Tyr	Met	Gly	Leu	Pro	Gly	Ile
164					680					685					690
166	Gln	Gly	Lys	Lys	Gly	Asp	Lys	Gly	Asn	Gln	Gly	Glu	Lys	Gly	Ile
167					695					700					705
169	Gln	Gly	Gln	Lys	Gly	Glu	Asn	Gly	Arg	Gln	Gly	Ile	Pro	Gly	Gln
170					710					715					720
172	Gln	Gly	Ile	Gln	Gly	His	His	Gly	Ala	Lys	Gly	Glu	Arg	Gly	Glu
173					725					730					735
175	Lys	Gly	Glu	Pro	Gly	Val	Arg	Gly	Ala	Ile	Gly	Ser	Lys	Gly	Glu
176					740					745					750
178	Ser	Gly	Val	Asp	Gly	Leu	Met	Gly	Pro	Ala	Gly	Pro	Lys	Gly	Gln
179					755					760					765
181	Pro	Gly	Asp	Pro	Gly	Pro	Gln	Gly	Pro	Pro	Gly	Leu	Asp	Gly	Lys
182					770					775					780
184	Pro	Gly	Arg	Glu	Phe	Ser	Glu	Gln	Phe	Ile	Arg	Gln	Val	Cys	Thr
185					785					790					795
187	Asp	Val	Ile	Arg	Ala	Gln	Leu	Pro	Val	Leu	Leu	Gln	Ser	Gly	Arg
188					800					805					810
190	Ile	Arg	Asn	Cys	Asp	His	Cys	Leu	Ser	Gln	His	Gly	Ser	Pro	Gly
191					815					820					825
193	Ile	Pro	Gly	Pro	Pro	Gly	Pro	Ile	Gly	Pro	Glu	Gly	Pro	Arg	Gly
194					830					835					840
196	Leu	Pro	Gly	Leu	Pro	Gly	Arg	Asp	Gly	Val	Pro	Gly	Leu	Val	Gly
197					845					850					855
199	Val	Pro	Gly	Arg	Pro	Gly	Val	Arg	Gly	Leu	Lys	Gly	Leu	Pro	Gly
200					860					865					870
202	Arg	Asn	Gly	Glu	Lys	Gly	Ser	Gln	Gly	Phe	Gly	Tyr	Pro	Gly	Glu
203					875					880					885
205	Gln	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Glu	Gly	Pro	Pro	Gly	Ile
206					890					895					900
208	Ser	Lys	Glu	Gly	Pro	Pro	Gly	Asp	Pro	Gly	Leu	Pro	Gly	Lys	Asp
209					905					910					915
211	Gly	Asp	His	Gly	Lys	Pro	Gly	Ile	Gln	Gly	Gln	Pro	Gly	Pro	Pro

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212          920          925          930
214 Gly Ile Cys Asp Pro Ser Leu Cys Phe Ser Val Ile Ala Arg Arg
215          935          940          945
217 Asp Pro Phe Arg Lys Gly Pro Asn Tyr
218          950
220 <210> SEQ ID NO: 2
221 <211> LENGTH: 171
222 <212> TYPE: PRT
223 <213> ORGANISM: Homo sapiens
225 <220> FEATURE:
226 <223> OTHER INFORMATION: von Willebrand factor A domain
228 <400> SEQUENCE: 2
229 Asp Leu Val Phe Ile Leu Asp Gly Ser Tyr Ser Val Gly Pro Glu
230 1          5          10          15
232 Asn Phe Glu Ile Val Lys Lys Trp Leu Val Asn Ile Thr Lys Asn
233          20          25          30
235 Phe Asp Ile Gly Pro Lys Phe Ile Gln Val Gly Val Val Gln Tyr
236          35          40          45
238 Ser Asp Tyr Pro Val Leu Glu Ile Pro Leu Gly Ser Tyr Asp Ser
239          50          55          60
241 Gly Glu His Leu Thr Ala Ala Val Glu Ser Ile Leu Tyr Leu Gly
242          65          70          75
244 Gly Asn Thr Lys Thr Gly Lys Ala Ile Gln Phe Ala Leu Asp Tyr
245          80          85          90
247 Leu Phe Ala Lys Ser Ser Arg Phe Leu Thr Lys Ile Ala Val Val
248          95          100          105
250 Leu Thr Asp Gly Lys Ser Gln Asp Asp Val Lys Asp Ala Ala Gln
251          110          115          120
253 Ala Ala Arg Asp Ser Lys Ile Thr Leu Phe Ala Ile Gly Val Gly
254          125          130          135
256 Ser Glu Thr Glu Asp Ala Glu Leu Arg Ala Ile Ala Asn Lys Pro
257          140          145          150
259 Ser Ser Thr Tyr Val Phe Tyr Val Glu Asp Tyr Ile Ala Ile Ser
260          155          160          165
262 Lys Ile Arg Glu Val Met
263          170
266 <210> SEQ ID NO: 3
267 <211> LENGTH: 183
268 <212> TYPE: PRT
269 <213> ORGANISM: Homo sapiens
271 <220> FEATURE:
272 <223> OTHER INFORMATION: Thrombospondin N-terminal-like domain
274 <400> SEQUENCE: 3
275 Gly Phe Asp Ile Leu Leu Gly Leu Asp Val Asn Lys Lys Val Lys
276 1          5          10          15
278 Lys Arg Ile Gln Leu Ser Pro Lys Lys Ile Lys Gly Tyr Glu Val
279          20          25          30
281 Thr Ser Lys Val Asp Leu Ser Glu Leu Thr Ser Asn Val Phe Pro
282          35          40          45

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```

284 Glu Gly Leu Pro Pro Ser Tyr Val Phe Val Ser Thr Gln Arg Phe
285                      50                      55                      60
287 Lys Val Lys Lys Ile Trp Asp Leu Trp Arg Ile Leu Thr Ile Asp
288                      65                      70                      75
290 Gly Arg Pro Gln Ile Ala Val Thr Leu Asn Gly Val Asp Lys Ile
291                      80                      85                      90
293 Leu Leu Phe Thr Thr Thr Ser Val Ile Asn Gly Ser Gln Val Val
294                      95                      100                     105
296 Thr Phe Ala Asn Pro Gln Val Lys Thr Leu Phe Asp Glu Gly Trp
297                      110                     115                     120
299 His Gln Ile Arg Leu Leu Val Thr Glu Gln Asp Val Thr Leu Tyr
300                      125                     130                     135
302 Ile Asp Asp Gln Gln Ile Glu Asn Lys Pro Leu His Pro Val Leu
303                      140                     145                     150
305 Gly Ile Leu Ile Asn Gly Gln Thr Gln Ile Gly Lys Tyr Ser Gly
306                      155                     160                     165
308 Lys Glu Glu Thr Val Gln Phe Asp Val Gln Lys Leu Arg Ile Tyr
309                      170                     175                     180
311 Cys Asp Pro
315 <210> SEQ ID NO: 4
316 <211> LENGTH: 509
317 <212> TYPE: PRT
318 <213> ORGANISM: Homo sapiens
320 <220> FEATURE:
321 <223> OTHER INFORMATION: collagenous domain
322     Pro in this sequence stands for hydroxyproline
324 <400> SEQUENCE: 4
325 Gly Lys Pro Gly Leu Gln Gly Pro Lys Gly Asp Pro Gly Leu Pro
326 1                      5                      10                      15
328 Gly Asn Pro Gly Tyr Pro Gly Gln Pro Gly Gln Asp Gly Lys Pro
329                      20                      25                      30
331 Gly Tyr Gln Gly Ile Ala Gly Thr Pro Gly Val Pro Gly Ser Pro
332                      35                      40                      45
334 Gly Ile Gln Gly Ala Arg Gly Leu Pro Gly Tyr Lys Gly Glu Pro
335                      50                      55                      60
337 Gly Arg Asp Gly Asp Lys Gly Asp Arg Gly Leu Pro Gly Phe Pro
338                      65                      70                      75
340 Gly Leu His Gly Met Pro Gly Ser Lys Gly Glu Met Gly Ala Lys
341                      80                      85                      90
343 Gly Asp Lys Gly Ser Pro Gly Phe Tyr Gly Lys Lys Gly Ala Lys
344                      95                      100                     105
346 Gly Glu Lys Gly Asn Ala Gly Phe Pro Gly Leu Pro Gly Pro Ala
347                      110                     115                     120
349 Gly Glu Pro Gly Arg His Gly Lys Asp Gly Leu Met Gly Ser Pro
350                      125                     130                     135
352 Gly Phe Lys Gly Glu Ala Gly Ser Pro Gly Ala Pro Gly Gln Asp
353                      140                     145                     150
355 Gly Thr Arg Gly Glu Pro Gly Ile Pro Gly Phe Pro Gly Asn Arg
356                      155                     160                     165

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VERIFICATION SUMMARY

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L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date